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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/531,438

DATE: 04/05/2001
 TIME: 08:26:29

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3 <110> APPLICANT: GILBERT, MARYSE
 4 POPOFF, MICHEL-ROBERT
 6 <120> TITLE OF INVENTION: CLOSTRIDIUM TOXIN AND PROCESS FOR THE PREPARATION OF IMMUNOGENIC
 7 COMPOSITIONS
 9 <130> FILE REFERENCE: 0660-0172-0CONT
 11 <140> CURRENT APPLICATION NUMBER: 09/531,438
 12 <141> CURRENT FILING DATE: 2000-03-20
 14 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01999
 15 <151> PRIOR FILING DATE: 1998-09-17
 17 <150> PRIOR APPLICATION NUMBER: FR971170
 18 <151> PRIOR FILING DATE: 1997-09-17
 20 <160> NUMBER OF SEQ ID NOS: 7
 22 <170> SOFTWARE: PatentIn version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1392
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Clostridium perfringens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (268)..(1065)
 33 <400> SEQUENCE: 1
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 38 aaagtgttct cgggggacac tttttgtttt taaaaaggaa aatataaata aaatttagat 180
 40 aaaagtgtaa aataattatt tttattttaa atttgttaaa aatttgatat aattgaattg 240
 42 taaaaaaaaat ttcagggggg aatataa atg aaa aaa att att tca aag ttt act 294
 43 Met Lys Lys Ile Ile Ser Lys Phe Thr
 44 1 5
 46 gta att ttt atg ttt tca tgt ttt ctt att gtt gga gca ata agt cca 342
 47 Val Ile Phe Met Phe Ser Cys Phe Leu Ile Val Gly Ala Ile Ser Pro
 48 10 15 20 25
 50 atg aaa gca agt gca aaa gaa atc gac gct tat aga aag gta atg gag 390
 51 Met Lys Ala Ser Ala Lys Glu Ile Asp Ala Tyr Arg Lys Val Met Glu
 52 30 35 40
 54 aat tat ctt aat gct tta aaa aac tac gat att aat aca gtt gta aac 438
 55 Asn Tyr Leu Asn Ala Leu Lys Asn Tyr Asp Ile Asn Thr Val Val Asn
 56 45 50 55
 58 att tca gaa gat gaa aga gta aat aat gtt gaa cag tat aga gaa atg 486
 59 Ile Ser Glu Asp Glu Arg Val Asn Asn Val Glu Gln Tyr Arg Glu Met
 60 60 65 70
 62 tta gaa gat ttt aaa tat gat cct aac caa caa ctg aaa tct ttt gaa 534
 63 Leu Glu Asp Phe Lys Tyr Asp Pro Asn Gln Gln Leu Lys Ser Phe Glu
 64 75 80 85
 66 ata ctt aat tca caa aag agc gat aat aaa gaa ata ttt aat gta aaa 582
 67 Ile Leu Asn Ser Gln Lys Ser Asp Asn Lys Glu Ile Phe Asn Val Lys
 68 90 95 100 105
 70 act gaa ttt tta aat ggt gca att tat gat atg gaa ttt act gta tca 630

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71 Thr Glu Phe Leu Asn Gly Ala Ile Tyr Asp Met Glu Phe Thr Val Ser
72          110          115          120
74 tct aaa gat gga aaa tta ata gta tct gat atg gaa aga aca aaa gtt      678
75 Ser Lys Asp Gly Lys Leu Ile Val Ser Asp Met Glu Arg Thr Lys Val
76          125          130          135
78 gag aat gaa gga aaa tat att tta aca cca tca ttt aga act caa gtt      726
79 Glu Asn Glu Gly Lys Tyr Ile Leu Thr Pro Ser Phe Arg Thr Gln Val
80          140          145          150
82 tgt aca tgg gat gat gaa cta gca caa gca att ggg gga gtt tat cca      774
83 Cys Thr Trp Asp Asp Glu Leu Ala Gln Ala Ile Gly Gly Val Tyr Pro
84          155          160          165
86 caa aca tat tct gat aga ttt aca tat tat gca gat aat ata tta tta      822
87 Gln Thr Tyr Ser Asp Arg Phe Thr Tyr Tyr Ala Asp Asn Ile Leu Leu
88 170          175          180          185
90 aac ttc aga caa tat gca act tca ggt tca aga gat tta aaa gta gaa      870
91 Asn Phe Arg Gln Tyr Ala Thr Ser Gly Ser Arg Asp Leu Lys Val Glu
92          190          195          200
94 tat agt gtt gta gat cat tgg atg tgg aaa gat gat gtt aaa gct tct      918
95 Tyr Ser Val Val Asp His Trp Met Trp Lys Asp Asp Val Lys Ala Ser
96          205          210          215
98 caa atg gta tat ggt caa aat cct gat tct gct aga caa ata aga tta      966
99 Gln Met Val Tyr Gly Gln Asn Pro Asp Ser Ala Arg Gln Ile Arg Leu
100          220          225          230
102 tat ata gaa aaa gga caa tct ttc tat aaa tat aga ata aga att aaa      1014
103 Tyr Ile Glu Lys Gly Gln Ser Phe Tyr Lys Tyr Arg Ile Arg Ile Lys
104          235          240          245
106 aac ttt aca cct gca tca att aga gta ttt ggt gaa ggg tat tgt gca      1062
107 Asn Phe Thr Pro Ala Ser Ile Arg Val Phe Gly Glu Gly Tyr Cys Ala
108 250          255          260          265
110 tag aaaaaaatat gaagtgcactt agtcacttca tttttttttt actattaatt      1115
112 ttattatata aaacctaac atacatgaaa gtattcttaa tacagttata tcaaaattaa      1175
114 agtaggggaa ataaaataaa aggctaaaaa ctatattaaa aactataaaa attattaaat      1235
116 taggttttaa ggtgttatat ttatttatga ttataggaat aaatatgcca aatggaataa      1295
118 ataaaagtaa tattaataat tgggtctaaaa agtatacatc attgataaaa gaaaaattac      1355
120 cagtaaaaaat tgagcttaaa aaattaaatg taaattt      1392
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 265
125 <212> TYPE: PRT
126 <213> ORGANISM: Clostridium perfringens
128 <400> SEQUENCE: 2
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134 Phe Leu Ile Val Gly Ala Ile Ser Pro Met Lys Ala Ser Ala Lys Glu
135          20          25          30
138 Ile Asp Ala Tyr Arg Lys Val Met Glu Asn Tyr Leu Asn Ala Leu Lys
139          35          40          45
142 Asn Tyr Asp Ile Asn Thr Val Val Asn Ile Ser Glu Asp Glu Arg Val
143          50          55          60
146 Asn Asn Val Glu Gln Tyr Arg Glu Met Leu Glu Asp Phe Lys Tyr Asp

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147 65          70          75          80
150 Pro Asn Gln Gln Leu Lys Ser Phe Glu Ile Leu Asn Ser Gln Lys Ser
151          85          90          95
154 Asp Asn Lys Glu Ile Phe Asn Val Lys Thr Glu Phe Leu Asn Gly Ala
155          100          105          110
158 Ile Tyr Asp Met Glu Phe Thr Val Ser Ser Lys Asp Gly Lys Leu Ile
159          115          120          125
162 Val Ser Asp Met Glu Arg Thr Lys Val Glu Asn Glu Gly Lys Tyr Ile
163          130          135          140
166 Leu Thr Pro Ser Phe Arg Thr Gln Val Cys Thr Trp Asp Asp Glu Leu
167 145          150          155          160
170 Ala Gln Ala Ile Gly Gly Val Tyr Pro Gln Thr Tyr Ser Asp Arg Phe
171          165          170          175
174 Thr Tyr Tyr Ala Asp Asn Ile Leu Leu Asn Phe Arg Gln Tyr Ala Thr
175          180          185          190
178 Ser Gly Ser Arg Asp Leu Lys Val Glu Tyr Ser Val Val Asp His Trp
179          195          200          205
182 Met Trp Lys Asp Asp Val Lys Ala Ser Gln Met Val Tyr Gly Gln Asn
183          210          215          220
186 Pro Asp Ser Ala Arg Gln Ile Arg Leu Tyr Ile Glu Lys Gly Gln Ser
187 225          230          235          240
190 Phe Tyr Lys Tyr Arg Ile Arg Ile Lys Asn Phe Thr Pro Ala Ser Ile
191          245          250          255
194 Arg Val Phe Gly Glu Gly Tyr Cys Ala
195          260          265
198 <210> SEQ ID NO: 3
199 <211> LENGTH: 327
200 <212> TYPE: DNA
201 <213> ORGANISM: Clostridium perfringens
203 <400> SEQUENCE: 3
204 atttgggata tcttaaattt agcacagaag aatgttttaa tgaaataaag ataataaaaa 60
206 gatatatataa ttatatagct gaaaatttat aattatatga taagtatagt taataaataa 120
208 aaagtgttct cgggggacac ttttttgttt taaaaaggaa aatataaata aaatttagat 180
210 aaaagtgtaa aataattatt tttattttaa atttgttaa aatttgatat aattgaattg 240
212 taaaaaaaaat ttcagggggg aatataaatg aaaaaaatta tttcaaagtt tactgtaatt 300
214 tttatgtttt catgttttct tattgtt 327
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 90
219 <212> TYPE: DNA
220 <213> ORGANISM: Clostridium perfringens
222 <220> FEATURE:
223 <221> NAME/KEY: CDS
224 <222> LOCATION: (1)..(90)
226 <400> SEQUENCE: 4
227 atg aaa aaa att att tca aag ttt act gta att ttt atg ttt tca tgt 48
228 Met Lys Lys Ile Ile Ser Lys Phe Thr Val Ile Phe Met Phe Ser Cys
229 1          5          10          15
231 ttt ctt att gtt gga gca ata agt cca atg aaa gca agt gca 90
232 Phe Leu Ile Val Gly Ala Ile Ser Pro Met Lys Ala Ser Ala

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238 <212> TYPE: PRT
239 <213> ORGANISM: Clostridium perfringens
241 <400> SEQUENCE: 5
243 Met Lys Lys Ile Ile Ser Lys Phe Thr Val Ile Phe`Met Phe Ser Cys
244 1                               5                               10                               15
247 Phe Leu Ile Val Gly Ala Ile Ser Pro Met Lys Ala Ser Ala
248                               20                               25                               30
251 <210> SEQ ID NO: 6
252 <211> LENGTH: 30
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <221> NAME/KEY: misc_feature
258 <223> OTHER INFORMATION: synthetic DNA
261 <400> SEQUENCE: 6
262 gaaatgttta caactgtatt aatatcgtag                               30
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266 <211> LENGTH: 23
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <221> NAME/KEY: misc_feature
272 <223> OTHER INFORMATION: synthetic DNA
275 <400> SEQUENCE: 7
276 tcaagtttgt acatgggatg atg                               23

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